

Claims

1. A description method of an alignment information characterized by the separation of an alignment information on an amino-acid sequence or a nucleic-acid sequence into a sequence information and a gap information expressing correspondence between sequences.

2. A storing method of an alignment information characterized by the separation of an alignment information on an amino-acid sequence or a nucleic-acid sequence into a sequence information and a gap information expressing correspondence between sequences, and wherein each information is stored and/or searched in one or more storage devices.

3. The method according to claim 2 which stores at least the gap information in one or more storage device.

4. The method according to claim 2 which stores only the gap information.

5. The method according to any one of claims 1 to 4, in which the gap information is described by using the residue number and/or the number of residues which indicates the location and the length of a gap region existing in the alignment information of more than two sequences, or a numerical data convertible to those numbers by calculation.

6. The method according to any one of claims 1 to 4, in which the gap information is described by using a data containing the residue number of another sequence not included in the alignment or a virtual sequence or column number of a standard representation

of the alignment information or a numerical data convertible by calculation to the data.

7. A method of generating a gap information of a new alignment information by calculation on only a gap information generated from an information of one or more alignments by any one of the methods according to claims 1 to 6.

8. A method of obtaining a standard representation of an alignment information from both a gap information and a sequence information obtained by the method according to any one of claims 1 to 7.

9. A communication method of an alignment information characterized by the separation of an alignment information on an amino-acid sequence or a nucleic-acid sequence to a sequence information and a gap information expressing correspondence between sequences, and by the communication of the gap information at least out of the informations.

10. The method according to claim 9 in which redundancy of the sequence information is removed prior to communication and necessary minimum of the sequence information is transferred.

11. A method of determining a substantially unique identifier of an alignment information, wherein the identifier is determined using and depending on only and all of a data on a gap information and identifiers of sequences in a sequence information.

12. A data record including at least its identifier and a gap information and identifiers of sequences in a sequence information generated by the method according to any one of claims 1 to 10, and a media containing one or more of the record.

13. The data record according to claim 12, wherein its identifier is generated by the method according to claim 11.

14. A method of storing, searching and/or communicating method of an alignment information which employs at least the data record according to claim 12 or claim 13.

15. The method according to any one of claims 1 to 14 which employs the correspondence information instead of the gap information.

16. The method according to any one of claims 1 to 15 which employs eigen-identifier of sequences in the sequence information.

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